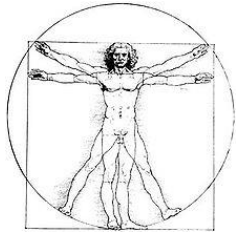


GEO Submissions and Usage

Stephen Wilhite (wilhite@nih.gov)

NCBI Genome Resources Workshop

PAG XXVII January 14, 2019

U.S. National Library of Medicine
National Center for Biotechnology Information

Why GEO?

- Permanent archiving/increased visibility & value/data sharing
- Publishing your results
- Digging into published data sets
- Exploring what's already available (new discoveries; support findings)

Common study types in functional genomics

Functional genomics experiments measure changes in the DNA (genome and epigenome), RNA (transcriptome), or interactions between DNA/RNA and proteins that influence the phenotype of a sample. Common branches of functional genomics include (Figure 7):

- genotyping;
- transcription profiling;
- epigenetic profiling;
- nucleic acid-protein interactions;
- meta-analysis.

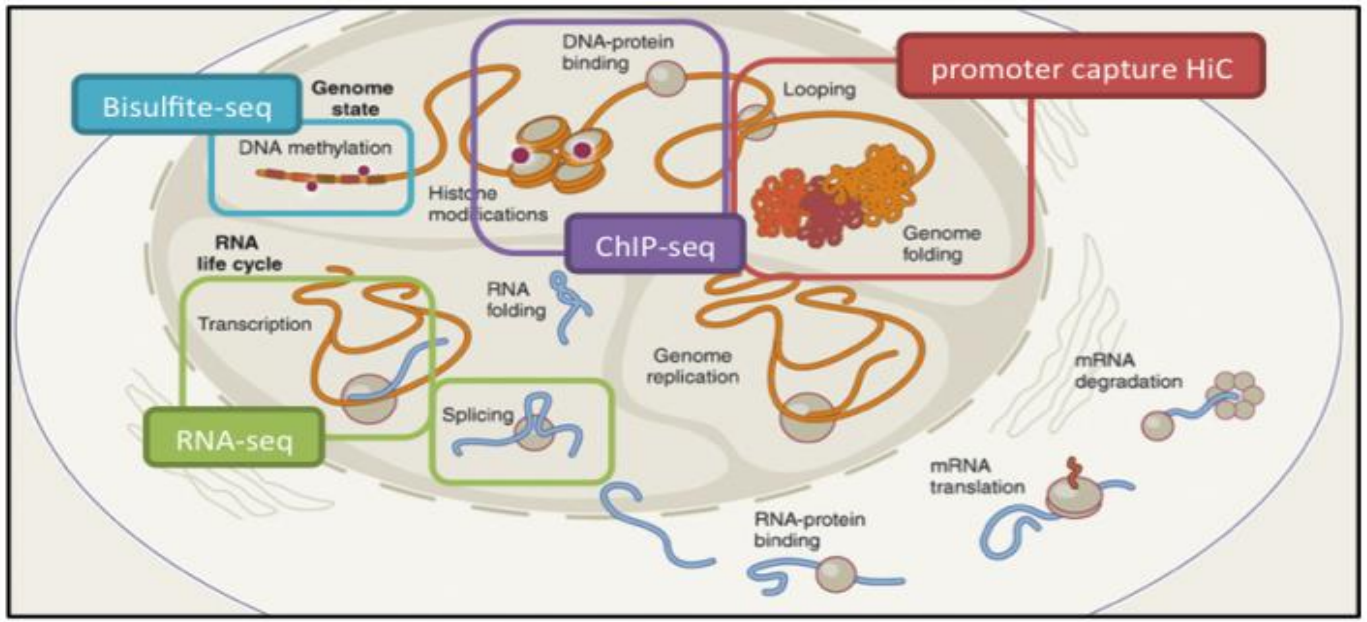
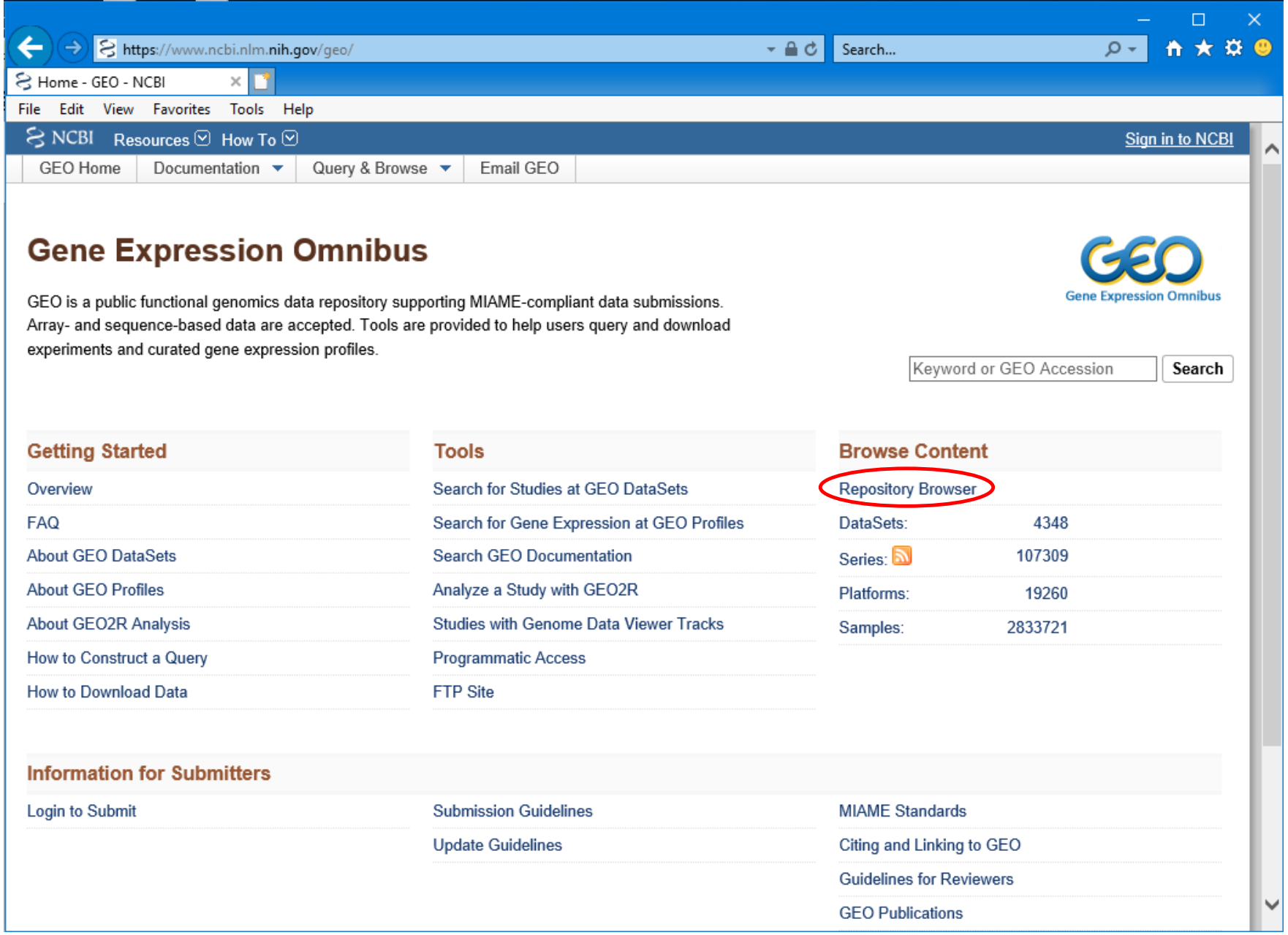


Figure 7 The molecules that can be analysed by functional genomics and the technologies used in the analysis. Reprinted by permission from Macmillan Publishers Ltd: Nature Biotechnology. Shendure J and Lieberman E. The expanding scope of DNA sequencing. 30:1084-94, copyright 2012 (7).


https://www.ncbi.nlm.nih.gov/geo/
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GEO Home
Documentation
Query & Browse
Email GEO
Gene Expression Omnibus
GEO is a public functional genomics data repository supporting MIAME-compliant data submissions. Array- and sequence-based data are accepted. Tools are provided to help users query and download experiments and curated gene expression profiles.
Gene Expression Omnibus
Keyword or GEO Accession
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About GEO Profiles
About GEO2R Analysis
How to Construct a Query
How to Download Data
Tools
Search for Studies at GEO DataSets
Search for Gene Expression at GEO Profiles
Search GEO Documentation
Analyze a Study with GEO2R
Studies with Genome Data Viewer Tracks
Programmatic Access
FTP Site
Browse Content
Repository Browser
DataSets: 4348
Series: 107309
Platforms: 19260
Samples: 2833721
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MIAME Standards
Citing and Linking to GEO
Guidelines for Reviewers
GEO Publications

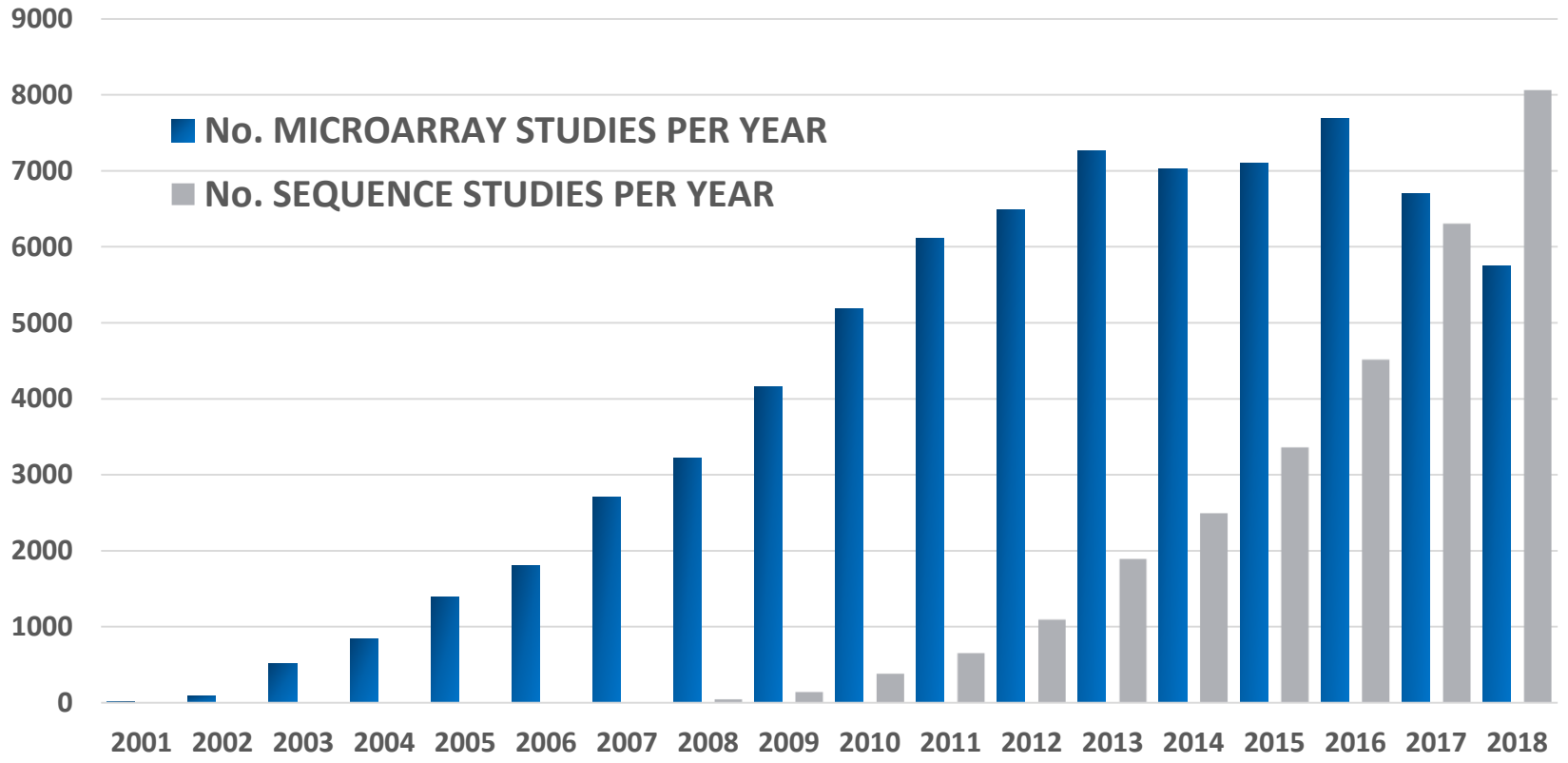
Public holdings

Series | Platforms | Samples | Organisms | History

Series type	Count
Expression profiling by array	56,484
Expression profiling by genome tiling array	735
Expression profiling by high throughput sequencing	23,458
Expression profiling by SAGE	239
Expression profiling by MPSS	20
Expression profiling by RT-PCR	634
Expression profiling by SNP array	14
Genome variation profiling by array	770
Genome variation profiling by genome tiling array	1,429
Genome variation profiling by high throughput sequencing	126
Genome variation profiling by SNP array	1,257
Genome binding/occupancy profiling by array	222
Genome binding/occupancy profiling by genome tiling array	2,304
Genome binding/occupancy profiling by high throughput sequencing	12,998
Genome binding/occupancy profiling by SNP array	17
Methylation profiling by array	920
Methylation profiling by genome tiling array	1,413
Methylation profiling by high throughput sequencing	2,253
Methylation profiling by SNP array	11
Protein profiling by protein array	268
Protein profiling by Mass Spec	6
SNP genotyping by SNP array	750
Other	4,068
Non-coding RNA profiling by array	3,795
Non-coding RNA profiling by genome tiling array	107
Non-coding RNA profiling by high throughput sequencing	3,502
Third-party reanalysis	311

Total holdings

	Public	Unreleased	Total
Series	107,310	12,600	119,910
Platforms	19,260	231	19,491
Samples	2,833,753	391,362	3,225,115


9000
8000
7000
6000
5000
4000
3000
2000
1000
0
No. MICROARRAY STUDIES PER YEAR
No. SEQUENCE STUDIES PER YEAR
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018

Public holdings

Series | Platforms | Samples | Organisms | History

See top organisms

Organism	Series	Platforms	Samples
Homo sapiens	45,027	5,393	1,539,972
Mus musculus	31,697	2,349	656,187
Rattus norvegicus	3,585	579	89,209
Drosophila melanogaster	3,350	366	58,560
Arabidopsis thaliana	3,731	378	53,390
Saccharomyces cerevisiae	2,573	600	52,799
Danio rerio	1,084	199	18,200
Sus scrofa	708	137	15,942
Caenorhabditis elegans	1,542	201	14,884
Bos taurus	784	189	14,124
Oryza sativa	738	193	11,491
Zea mays	401	114	11,051
Gallus gallus	663	137	10,125
Macaca mulatta	422	66	10,412
Canis lupus familiaris	272	63	8,614
synthetic construct	941	97	7,547
Escherichia coli	699	154	7,040
Glycine max	257	53	7,341
Schizosaccharomyces pombe	772	125	5,885
Plasmodium falciparum	195	63	6,186
Pimephales promelas	76	14	4,769
Vitis vinifera	172	37	4,255
Macaca fascicularis	96	22	3,943
Triticum aestivum	178	40	3,686
Ovis aries	200	47	3,109

Total holdings

	Public	Unreleased	Total
Series	107,334	12,644	119,978
Platforms	19,260	231	19,491
Samples	2,834,175	400,841	3,235,016

Citation listings: deposit and third-party usage

GEO third-party usage citations | GEO deposit citations

The following list represents third-party publications that cite GEO data as evidence to support or complement independent studies, or use GEO data as the basis of statistical/analytical hypotheses or tools. Please report omitted publications to geo@ncbi.nlm.nih.gov

Total number of citations: 7,160

Shin SH, Lee GY, Lee M, Kang J et al.
Aberrant expression of CITED2 promotes prostate cancer metastasis by activating the nucleolin-AKT pathway.
Nat Commun 2018 Oct 5;9(1):4113. PMID: 30291252

Chen J, Yu Y, Xue C, Chen X et al.
Low microRNA-139 expression associates with poor prognosis in patients with tumors: A meta-analysis.
Hepatobiliary Pancreat Dis Int 2018 Sep 26. PMID: 30290990

Li X, Li J, Wu P, Zhou L et al.
Smoker and non-smoker lung adenocarcinoma is characterized by distinct tumor immune microenvironments.
Oncoimmunology 2018;7(10):e1494677. PMID: 30288364

Wang W, Han T, Tong W, Zhao J et al.
Overexpression of GPR35 confers drug resistance in NSCLC cells by β-arrestin/Akt signaling.
Onco Targets Ther 2018;11:6249-6257. PMID: 30288060

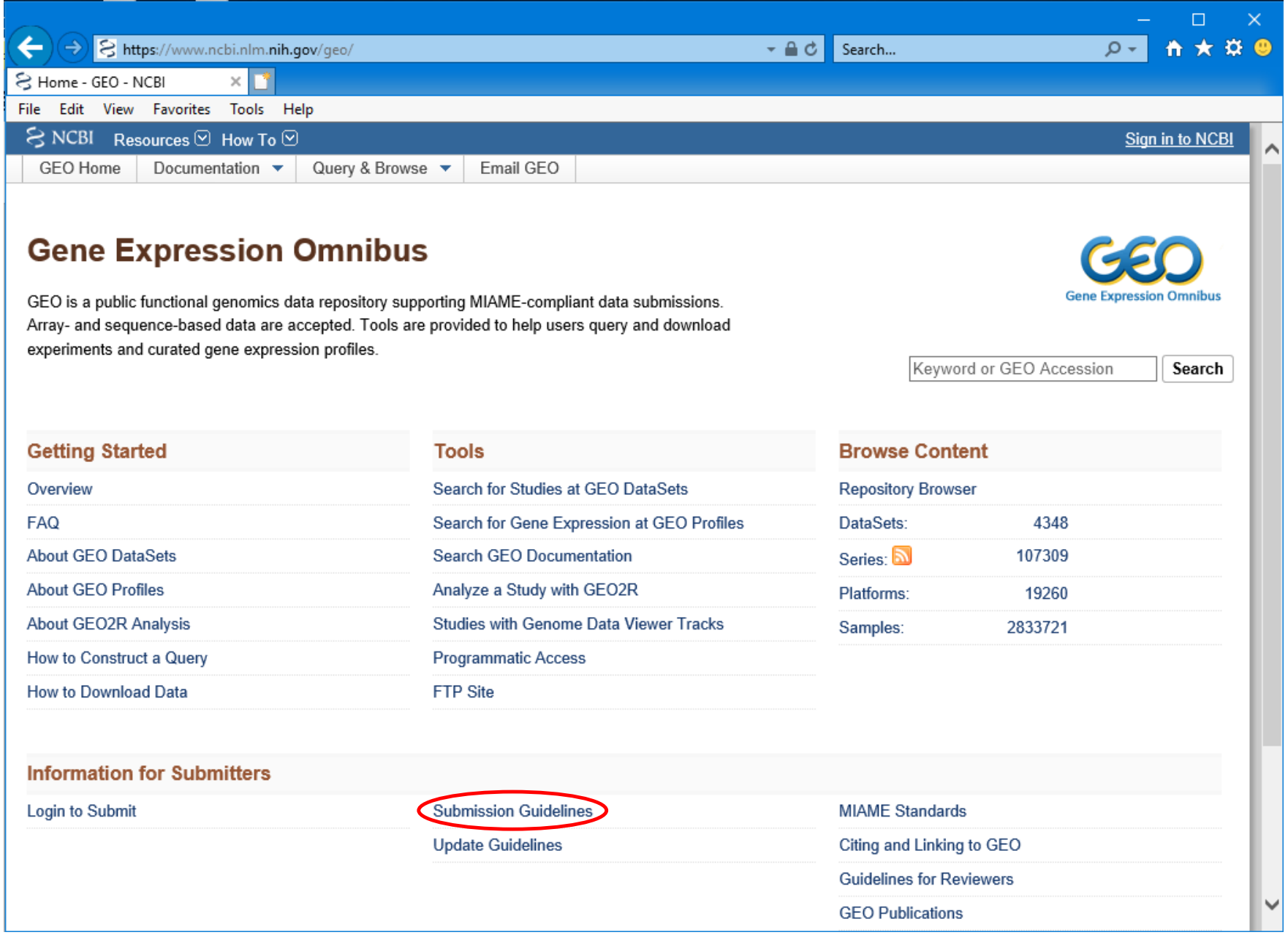
Wang Z, Qu H, Gong W, Liu A.
Up-regulation and tumor-promoting role of SPHK1 were attenuated by miR-330-3p in gastric cancer.
IUBMB Life 2018 Nov;70(11):1164-1176. PMID: 30281914

Squair JW, Tigchelaar S, Moon KM, Liu J et al.
Integrated systems analysis reveals conserved gene networks underlying response to spinal cord injury.
Elife 2018 Oct 2;7. PMID: 30277459

Yi Y, Liu Y, Wu W, Wu K et al.
The role of miR-106p-5p in cervical cancer: from expression to molecular mechanism.
Cell Death Discov 2018;4:36. PMID: 30275981

Holdings summary

- 107,000 studies (~350 studies/week)
- 2,800,000 samples (~10,000 samples/week)
- 4,400 organisms
- >55,000 primary data citations
- >7,000 third-party usage citations
- >36,000 unique submitters


https://www.ncbi.nlm.nih.gov/geo/
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Gene Expression Omnibus
GEO is a public functional genomics data repository supporting MIAME-compliant data submissions. Array- and sequence-based data are accepted. Tools are provided to help users query and download experiments and curated gene expression profiles.
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About GEO2R Analysis
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Submitting data

GEO accepts many categories of high-throughput functional genomic data, including all array-based applications and some high-throughput sequencing data.

We aim to make data deposit procedures as straightforward as possible and will provide as much assistance as you require to get your data submitted to GEO. If you have problems or questions about submission, e-mail us with a brief description of the type of data you are trying to submit, and one of our curators will quickly get back to you.

Data types

- Submit microarray
- Submit high-throughput sequencing
- Submit other (includes NanoString, RT-PCR, traditional SAGE)

WARNING: If you are submitting human data, it is your responsibility to comply with Human Subject Guidelines.

Fast facts

- Your final GEO records will be organized as illustrated at GEO Overview.
- See examples of the kinds of data GEO can accept.
- GEO supports various submission formats:
  - GEOarchive spreadsheet submissions are **recommended for most submitters**.
  - If your data and metadata are already in a database, and you can generate and export data in SOFT plain text or MINiML XML, you can use the GEO Direct deposit form to submit data.
- GEO accession numbers are normally approved within 5 business days after completion of submission. If you do not receive an e-mail from us within 5 business days of your submission, please first check your spam or junk e-mail folders because some systems recognize GEO e-mail correspondence as spam, then e-mail us to inquire about your submission.
- Your GEO submissions can remain private until a manuscript citing the data is published.
- You can allow reviewers anonymous access to your private records.
- You can update or edit your existing GEO records at any time.
- GEO supports MIAME- and MINSEQE-compliant data submissions.

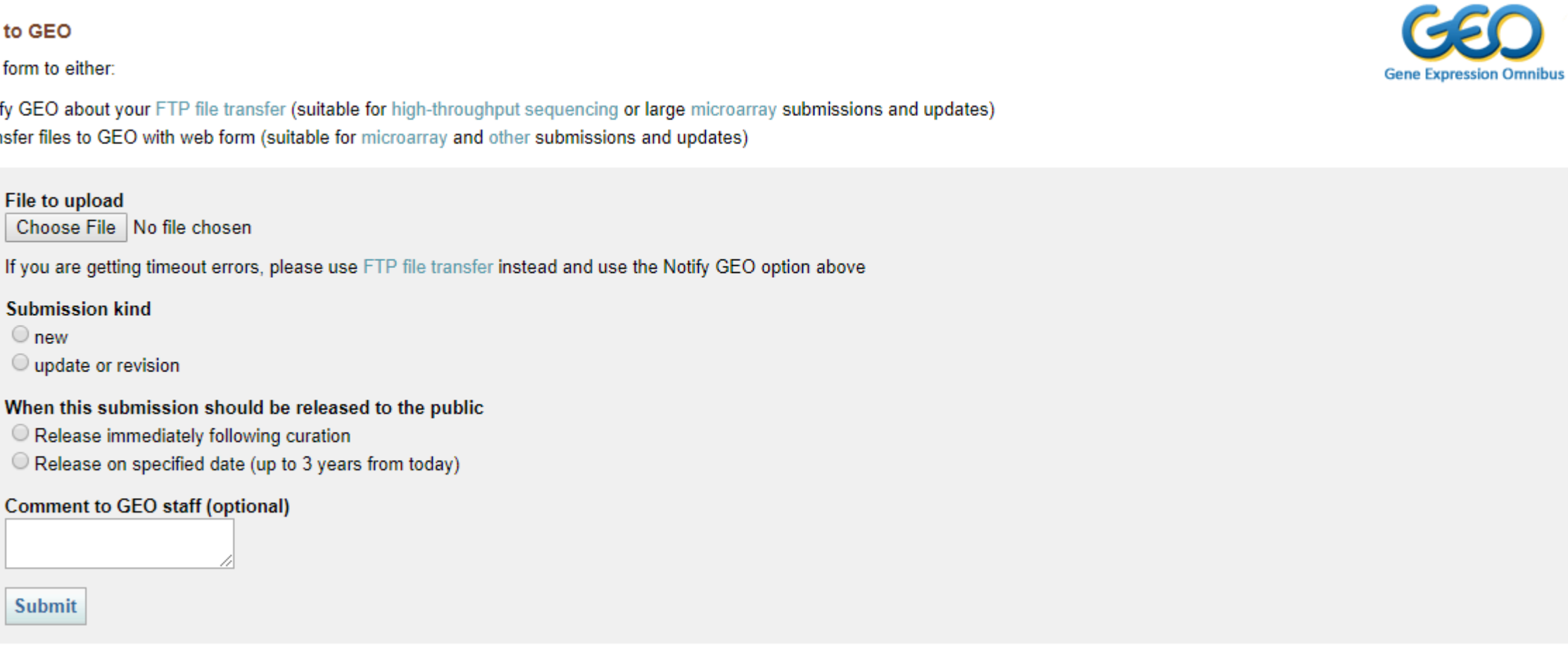
Submission factsheet!

Submission via metadata spreadsheet & data files

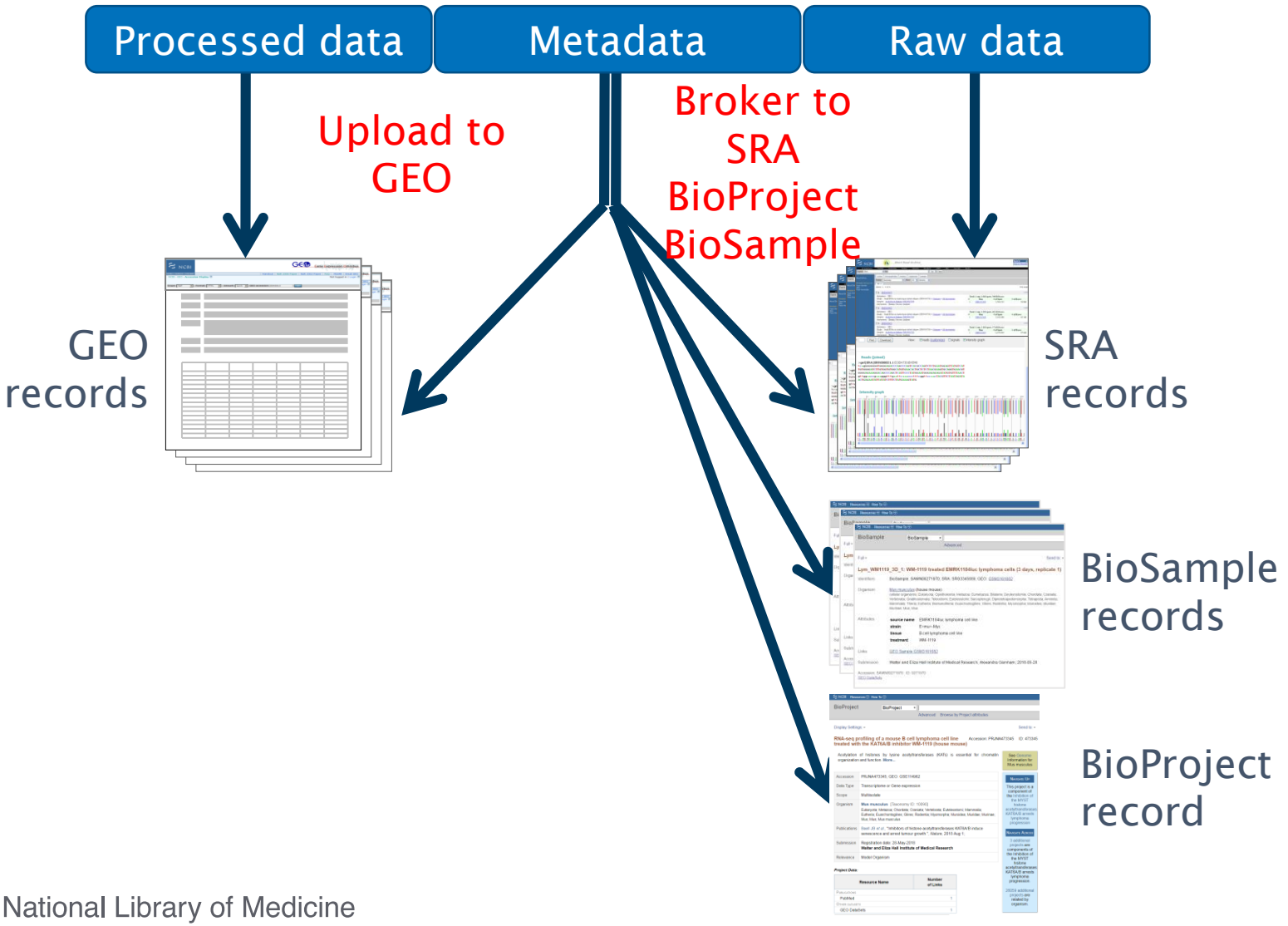
	A	B	C	D	E	F	G
1	SERIES						
2	# This section describes the overall experiment.						
3	title						
4	summary						
5	overall design						
6	contributor						
7	contributor						
8	supplementary file						
9							
10	SAMPLES						
11	# This section lists and describes each of the biological Samples under investgation, as well as any protocols that are specific to individual Samples.						
12	Sample name	title	source name	organism	characteristics: tag	characteristics: tag	characteristics: tag
13	Sample 1						
14	Sample 2						
15	Sample 3						
16							
17	PROTOCOLS						
18	# Any of the protocols below which are applicable to only a subset of Samples should be included as additional columns of the SAMPLES section instead.						
19	growth protocol						
20	treatment protocol						
21	extract protocol						
22	library construction protocol						
23	library strategy						
24							
25	DATA PROCESSING PIPELINE						
26	# Data processing steps include base-calling, alignment, filtering, peak-calling, generation of normalized abundance measurements etc...						
27	data processing step						
28	data processing step						
29	data processing step						
30	data processing step						
31	data processing step						
32	genome build						
33	processed data files format and content						
34							
35	# For each file listed in the "processed data file" columns of the SAMPLES section, provide additional information below.						
36	PROCESSED DATA FILES						
37	file name	file type	file checksum				
38							
39							
40							
41	# For each file listed in the "raw file" columns of the SAMPLES section, provide additional information below.						
42	RAW FILES						
43	file name	file type	file checksum	instrument model	read length	single or paired-end	
44							
45							
46							

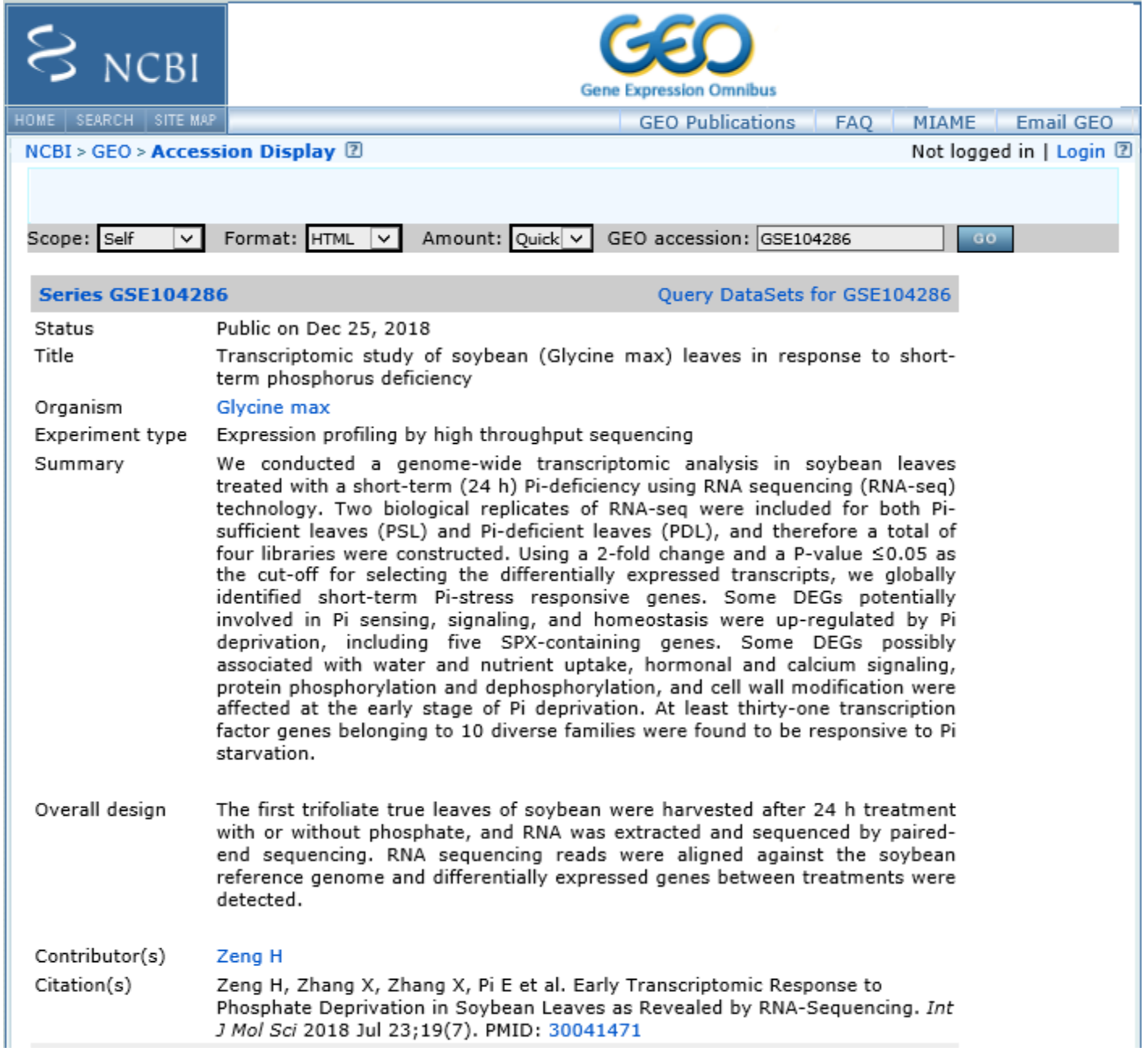
Submission via metadata spreadsheet & data files

	A	B	C	D	E	F	G
1	SERIES						
2	title	Genome-wide maps of chromatin state in pluripotent and lineage-committed cells.					
3	summary	We report the application of single-molecule-based sequencing technology for high-throughput profiling of histone modifications in mammalian cells. By obtaining over four billion bases of sequence from					
4	overall design	Examination of 2 different histone modifications in 2 cell types.					
5	contributor	John,B,Goode					
6	contributor	Bradley,Smith					
7	supplementary file						
8							
9	SAMPLES						
10	Sample name	title	source name	organism	characteristics: cell type	characteristics: passages	characteristics: strain
11	Sample 1	H3K4me2_ChIPSeq	Neural progenitor cells	Mus musculus	ES-derived neural progenitor cells	15-18	C57BL/6
12	Sample 2	H3K4me1_ChIPSeq	Neural progenitor cells	Mus musculus	ES-derived neural progenitor cells	15-18	C57BL/6
13	Sample 3	input DNA	Neural progenitor cells	Mus musculus	ES-derived neural progenitor cells	15-18	C57BL/6
14							
15	PROTOCOLS						
16	growth protocol	ES cell–derived NS cells were routinely generated by re-plating d 7 adherent neural differentiation cultures (typically 2–3 × 106 cells into a T75 flask) on uncoated plastic in NS-A medium (Euroclone, Mil					
17	extract protocol	Lysates were clarified from sonicated nuclei and histone-DNA complexes were isolated with antibody.					
18	library construction protocol	Libraries were prepared according to Illumina's instructions accompanying the DNA Sample Kit (Part# 0801-0303). Briefly, DNA was end-repaired using a combination of T4 DNA polymerase, E. coli DNA					
19	library strategy	ChIP-Seq					
20							
21	DATA PROCESSING PIPELINE						
22	data processing step	Basecalls performed using CASAVA version 1.4					
23	data processing step	ChIP-seq reads were aligned to the mm9 genome assembly using EasyAlign version 3.2 with the following configurations…					
24	data processing step	Data were filtered using the following specifications…					
25	data processing step	peaks were called using PeaksFind version 2.2 with the following setting: ChIP threshold (0.2), Enrichment Fold (2.5), Rescue Fold (3).					
26	data processing step						
27	genome build	mm9					
28	processed data files format and content	wig files were generated using …; Scores represent …					
29							
30	PROCESSED DATA FILES						
31	file name	file type	file checksum				
32	H3K4me2.peaks.wig	wig	95cf1d1fa509d871b2ef0bb9fd734c3d				
33	H3K4me1.peaks.wig	wig	8ec6ee3cce10b970e5bfea4e35cdb231				
34	H3K4me2.b.peaks.wig	wig	f8fcd650914ff1a733956d6d06e8b543				
35							
36	RAW FILES						
37	file name	file type	file checksum	instrument model	read length	single or paired-end	
38	080716_BI-EAS46_0001_209DH_L1.fastq	fastq	6cc6ee3cce10b970e5bfea4e35cdb	Illumina Genome Analyzer	36	single	
39	080716_BI-EAS46_0001_209DH_L2.fastq	fastq	88ceb0e0d056dda9208a03acf9073	Illumina Genome Analyzer	36	single	
40	080716_BI-EAS46_0001_209DH_L3.fastq	fastq	f2786fedc5106789a2af4014a0e74f(	Illumina Genome Analyzer	36	single	
41	080716_BI-EAS46_0001_209DH_L4.fastq	fastq	d8fcd650914ff1a733956d6d06e8b0	Illumina Genome Analyzer	36	single	
42	080716_BI-EAS46_0001_209DH_L5.fastq	fastq	03839cca2e797b28b9f9371f7b9ca(	Illumina Genome Analyzer	36	single	
43	080716_BI-EAS46_0001_209DH_L6.fastq	fastq	604fbb658413c559511eb6ad2bb14	Illumina Genome Analyzer	36	single	
44	080717_BI-EAS46_0001_20DH_L5.fastq	fastq	57cf1d1fa509d871b2ef0bb9fd734c3	Illumina Genome Analyzer IIx	42	single	
45	080717_BI-EAS46_0001_20DH_L6.fastq	fastq	e5718e1a97690d410464f24f37aae(	Illumina Genome Analyzer IIx	42	single	
46							


Submit to GEO
Use this form to either:
Notify GEO about your FTP file transfer (suitable for high-throughput sequencing or large microarray submissions and updates)
Transfer files to GEO with web form (suitable for microarray and other submissions and updates)
File to upload
Choose File
No file chosen
If you are getting timeout errors, please use FTP file transfer instead and use the Notify GEO option above
Submission kind
new
update or revision
When this submission should be released to the public
Release immediately following curation
Release on specified date (up to 3 years from today)
Comment to GEO staff (optional)
Submit

GEO <-> SRA, BioSample, BioProject





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Gene Expression Omnibus

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Not logged in | Login

Scope: Self | Format: HTML | Amount: Quick | GEO accession: GSE104286 | GO

Series GSE104286 Query DataSets for GSE104286

Status	Public on Dec 25, 2018
Title	Transcriptomic study of soybean (Glycine max) leaves in response to short-term phosphorus deficiency
Organism	Glycine max
Experiment type	Expression profiling by high throughput sequencing
Summary	We conducted a genome-wide transcriptomic analysis in soybean leaves treated with a short-term (24 h) Pi-deficiency using RNA sequencing (RNA-seq) technology. Two biological replicates of RNA-seq were included for both Pi-sufficient leaves (PSL) and Pi-deficient leaves (PDL), and therefore a total of four libraries were constructed. Using a 2-fold change and a P-value ≤0.05 as the cut-off for selecting the differentially expressed transcripts, we globally identified short-term Pi-stress responsive genes. Some DEGs potentially involved in Pi sensing, signaling, and homeostasis were up-regulated by Pi deprivation, including five SPX-containing genes. Some DEGs possibly associated with water and nutrient uptake, hormonal and calcium signaling, protein phosphorylation and dephosphorylation, and cell wall modification were affected at the early stage of Pi deprivation. At least thirty-one transcription factor genes belonging to 10 diverse families were found to be responsive to Pi starvation.
Overall design	The first trifoliate true leaves of soybean were harvested after 24 h treatment with or without phosphate, and RNA was extracted and sequenced by paired-end sequencing. RNA sequencing reads were aligned against the soybean reference genome and differentially expressed genes between treatments were detected.
Contributor(s)	Zeng H
Citation(s)	Zeng H, Zhang X, Zhang X, Pi E et al. Early Transcriptomic Response to Phosphate Deprivation in Soybean Leaves as Revealed by RNA-Sequencing. *Int J Mol Sci* 2018 Jul 23;19(7). PMID: 30041471

Platforms (1) GPL15008 Illumina HiSeq 2000 (Glycine max)

Samples (4) Less...
GSM2794349 Pi sufficient leaf-rep1
GSM2794350 Pi sufficient leaf-rep2
GSM2794351 Pi deficient leaf-rep1
GSM2794352 Pi deficient leaf-rep2

Relations

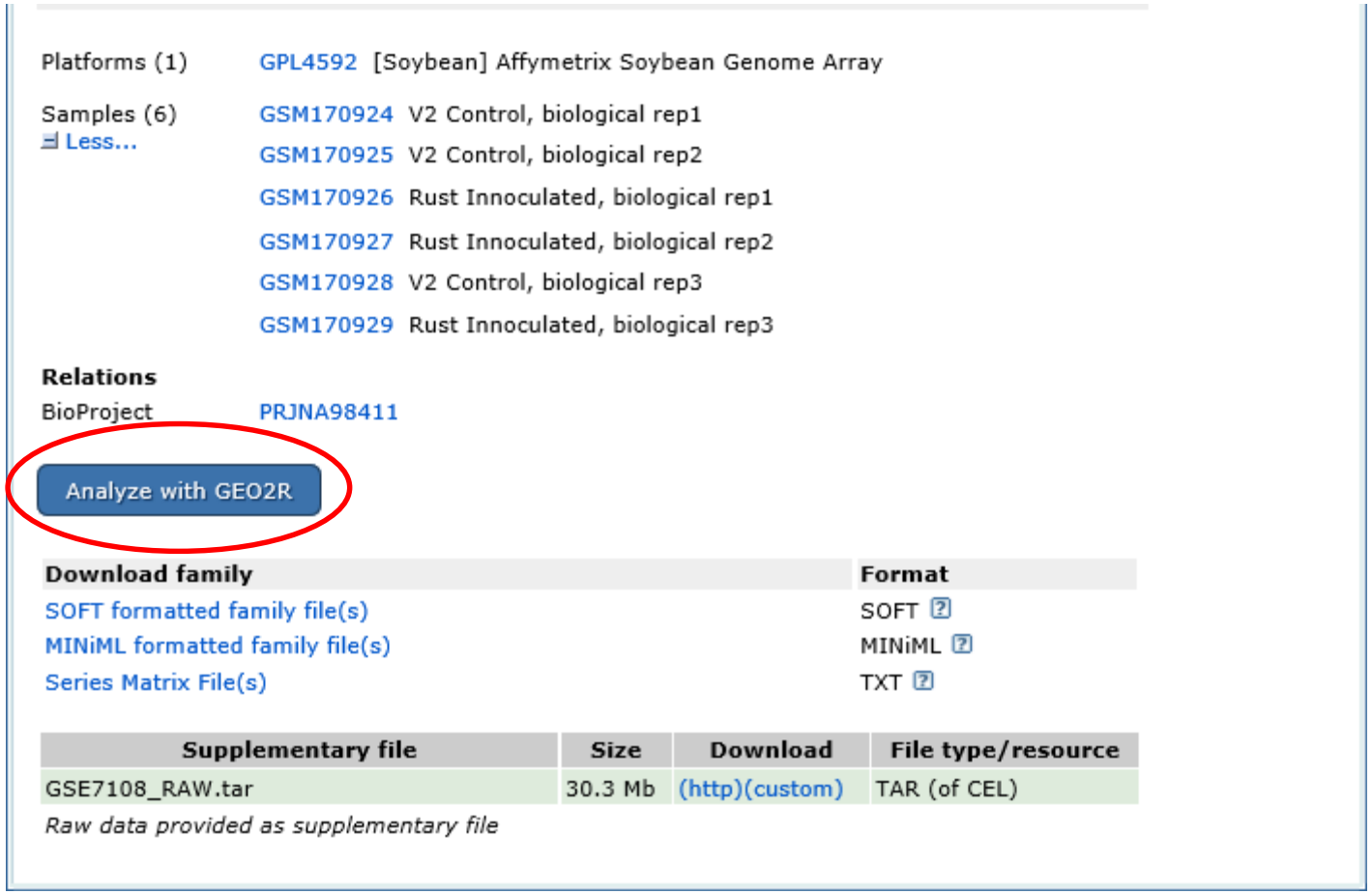
BioProject	PRJNA412240
SRA	SRP118921

Download family	Format
SOFT formatted family file(s)	SOFT
MINiML formatted family file(s)	MINiML
Series Matrix File(s)	TXT

Supplementary file	Size	Download	File type/resource
GSE104286_Gene_differential_expression.xlsx	7.8 Mb	(ftp)(http)	XLSX

Raw data are available in SRA

Processed data is available on Series record


Platforms (1) GPL4592 [Soybean] Affymetrix Soybean Genome Array
Samples (6)
Less...
GSM170924 V2 Control, biological rep1
GSM170925 V2 Control, biological rep2
GSM170926 Rust Innoculated, biological rep1
GSM170927 Rust Innoculated, biological rep2
GSM170928 V2 Control, biological rep3
GSM170929 Rust Innoculated, biological rep3
Relations
BioProject PRJNA98411
Analyze with GEO2R
Download family
Format
SOFT formatted family file(s)
SOFT
MINiML formatted family file(s)
MINiML
Series Matrix File(s)
TXT
Supplementary file
Size
Download
File type/resource
GSE7108_RAW.tar
30.3 Mb
(http)(custom)
TAR (of CEL)
Raw data provided as supplementary file

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Use GEO2R to compare two or more groups of Samples in order to identify genes that are differentially expressed across experimental conditions. Results are presented as a table of genes ordered by significance. Full instructions YouTube

GEO accession GSE7108 Set Gene expression analysis in soybean with respect to Pahakopsora pachyrhizii at V2 growth stage

Samples Define groups Selected **6** out of **6** samples

Columns Set

Group	Accession	Title	Source name	5601T unknown reaction to Asian soybean rust	Characteristics
V2 Control	GSM170924	V2 Control, biological rep1	Glycine max uninoculated leaf (Control)		Leaf samples collected 72 hours after inoculation from V2 growth stage)
V2 Control	GSM170925	V2 Control, biological rep2	Glycine max uninoculated leaf (Control)		Leaf samples collected 72 hours after inoculation from V2 growth stage)
V2 Control	GSM170928	V2 Control, biological rep3	Glycine max uninoculated leaf (Control)		Leaf samples collected 72 hours after inoculation from V2 growth stage)
Rust Innoculated	GSM170926	Rust Innoculated, biological rep1	Glycine max rust inoculated leaf (Treatment)		Leaf samples collected 72 hours after inoculation from V2 growth stage)
Rust Innoculated	GSM170927	Rust Innoculated, biological rep2	Glycine max rust inoculated leaf (Treatment)		Leaf samples collected 72 hours after inoculation from V2 growth stage)
Rust Innoculated	GSM170929	Rust Innoculated, biological rep3	Glycine max rust inoculated leaf (Treatment)		Leaf samples collected 72 hours after inoculation from V2 growth stage)

GEO2R | Value distribution | Options | Profile graph | R script

Quick start

- Specify a GEO Series accession and a Platform if prompted.
- Click 'Define groups' and enter names for the groups of Samples you plan to compare, e.g., test and control.
- Assign Samples to each group. Highlight Sample rows then click the group name to assign those Samples to the group. Use the Sample metadata (title, source and characteristics) columns to help determine which Samples belong to which group.
- Click 'Top 250' to perform the calculation with default settings.
- Results are presented as a table of genes ordered by significance. The top 250 genes are presented and may be viewed as profile graphs. Alternatively, the complete results table may be saved.
- You may change settings in Options tab.

How to use

Top 250 Save all results

Submission factsheet!

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NCBI » GEO » GEO2R » GSE7108 Login

Use GEO2R to compare two or more groups of Samples in order to identify genes that are differentially expressed across experimental conditions. Results are presented as a table of genes ordered by significance. Full instructions YouTube

GEO accession GSE7108 Set Gene expression analysis in soybean with respect to Pahakopsora pachyrhizii at V2 growth stage

▸ Samples ▸ Define groups Selected 6 out of 6 samples

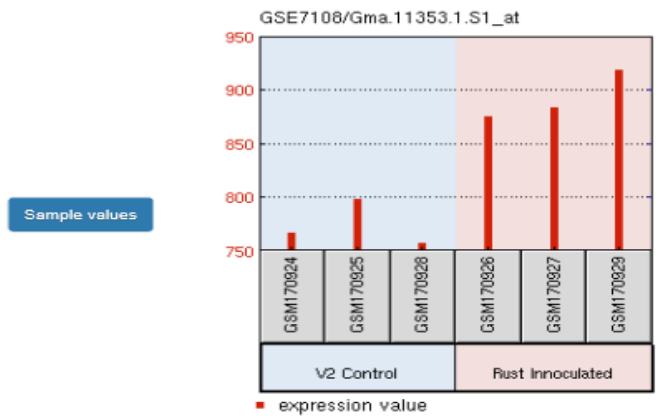
GEO2R | Value distribution | Options | Profile graph | R script

▸ Quick start

Log-transformation has been applied to the data. You can change this in the Options tab.

Recalculate if you changed any options. Save all results Select columns

ID	P.Value	logFC	GB_ACC
▸ Gma.7440.1.A1_at	0.0000294	-0.2004	BU547731
▸ Gma.16189.1.S1_at	0.0001439	0.3392	BQ742031
▸ GmaAffx.40402.1.S1_at	0.0006832	-0.3215	BF324415
▸ GmaAffx.31196.1.S1_at	0.0009181	0.8721	BE821537
▾ Gma.11353.1.S1_at	0.0015554	0.2051	AW397565
▸ Gma.2206.1.S1_at	0.0020967	-0.317	BG6



Submission factsheet!

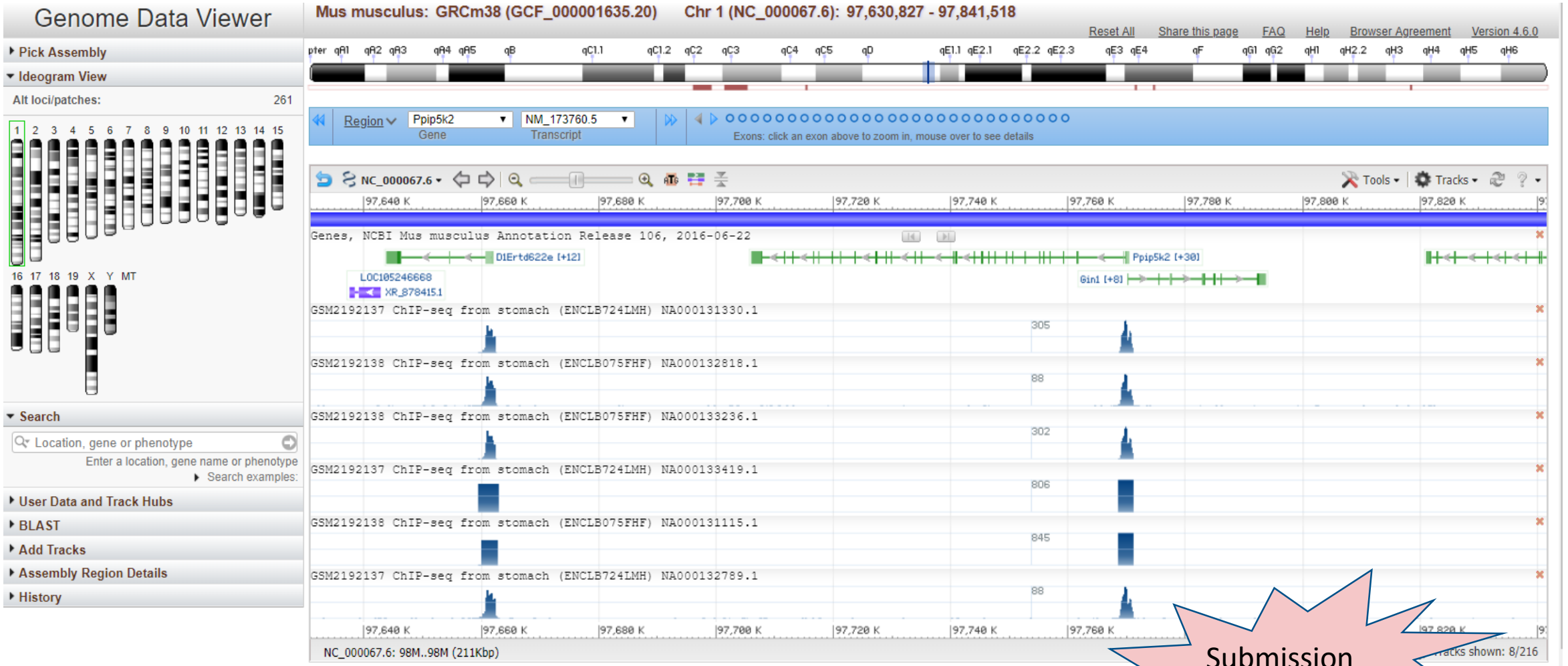
Platforms (1) GPL13112 Illumina HiSeq 2000 (Mus musculus)

Samples (2) GSM2192137 ChIP-seq from stomach (ENCLB724LMH)
GSM2192138 ChIP-seq from stomach (ENCLB075FHF)

See on Genome Data Viewer

Download family	Format
SOFT formatted family file(s)	SOFT
MINiML formatted family file(s)	MINiML
Series Matrix File(s)	TXT

Supplementary file	Size	Download	File type/resource
GSE82878_ENCFF283OBS_signal_p-value_mm10.bigWig	746.4 Mb	(ftp)(http)	BIGWIG
GSE82878_ENCFF309WXH_fold_change_over_control_mm10.bigWig	743.4 Mb	(ftp)(http)	BIGWIG
GSE82878_ENCFF533YRG_peaks_mm10.bed.gz	656.6 Kb	(ftp)(http)	BED
GSE82878_ENCFF569KWB_replicated_peaks_mm10.bed.gz	747.2 Kb	(ftp)(http)	BED
GSE82878_ENCFF708UMT_peaks_mm10.bigBed	1.9 Mb	(ftp)(http)	BIGBED
GSE82878_ENCFF849FYX_replicated_peaks_mm10.bigBed	1.7 Mb	(ftp)(http)	BIGBED
GSE82878_RAW.tar	1.8 Gb	(http)(custom)	TAR (of BED, BIGBED, BIGWIG, TXT)


Genome Data Viewer
Mus musculus: GRCm38 (GCF_000001635.20)
Chr 1 (NC_000067.6): 97,630,827 - 97,841,518
Reset All
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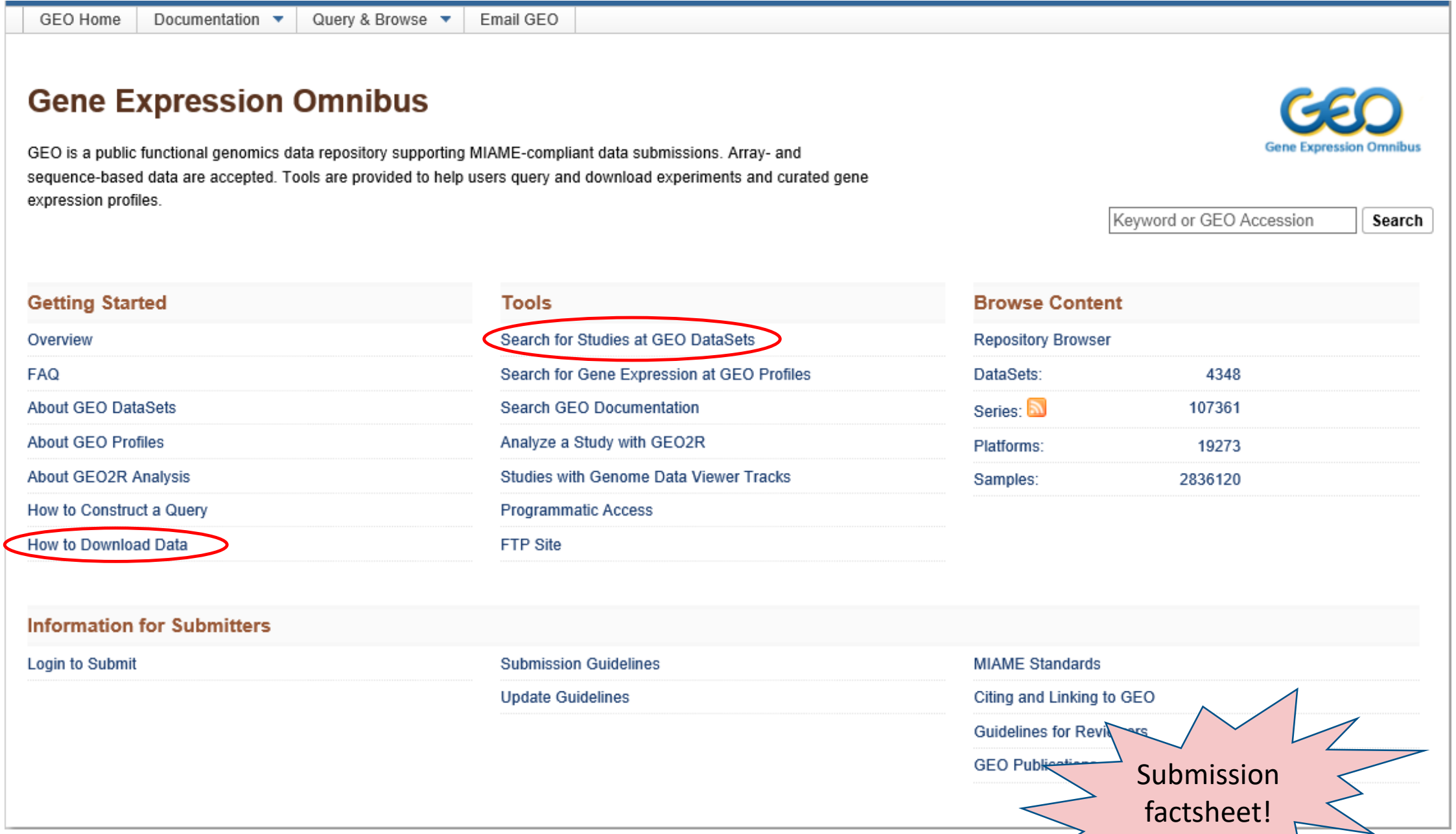
FAQ
Help
Browser Agreement
Version 4.6.0
Pick Assembly
Ideogram View
Alt loci/patches: 261
Region
Ppip5k2
Gene
NM_173760.5
Transcript
Exons: click an exon above to zoom in, mouse over to see details
NC_000067.6
Tools
Tracks
Genes, NCBI Mus musculus Annotation Release 106, 2016-06-22
D1Ertd622e [+12]
Ppip5k2 [+30]
LOC105246668
XR_878415.1
Gin1 [+8]
GSM2192137 ChIP-seq from stomach (ENCLB724LMH) NA000131330.1
GSM2192138 ChIP-seq from stomach (ENCLB075FHF) NA000132818.1
GSM2192138 ChIP-seq from stomach (ENCLB075FHF) NA000133236.1
GSM2192137 ChIP-seq from stomach (ENCLB724LMH) NA000133419.1
GSM2192138 ChIP-seq from stomach (ENCLB075FHF) NA000131115.1
GSM2192137 ChIP-seq from stomach (ENCLB724LMH) NA000132789.1
Search
Location, gene or phenotype
Enter a location, gene name or phenotype
Search examples:
User Data and Track Hubs
BLAST
Add Tracks
Assembly Region Details
History
NC_000067.6: 98M..98M (211Kbp)
Tracks shown: 8/216
Submission factsheet!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Platforms: 19273
Samples: 2836120
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MIAME Standards
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Guidelines for Revi
GEO Publica
Submission factsheet!

Thank you.

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Shelby Bidwell
Larissa Brown
Jianli Dai
Scott Durkin
Michel Eschenbrenner
Linda Frisse
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BioProject / Biosample
John Anderson
Carol Scott

GEO
Emily Clough
Carlos Evangelista
Irene Kim
Pierre Ledoux
Hyeseung Lee
Kimberly Marshall
Katherine Phillippy
Patti Sherman
Stephen Wilhite
Tanya Barrett

GEO developers
Alexandra Soboleva
Maxim Tomashevsky
Nadezhda Serova
Naigong Zhang

Annotation Pipeline
Francoise Thibaud-Nissen
Paul Kitts
Mike Dicuccio
Wratko Hlavina
Avi Kimchi

Jinna Choi
Patrick Masterson
Eyal Mozes
Robert Smith
Alexandre Souvorov

RefSeq/Gene
Eric Cox
Catherine Farrell
Tamara Goldfarb
Diana Haddad
John Jackson
Vinita Joardar
Kelly McGarvey
Michael Murphy
Nuala O'Leary

RefSeq Developers
Alex Astashyn
Olga Ermolaeva
Vamsi Kodali
Craig Wallin

Shashi Pujar
Bhanu Rajput
Sanjida Rangwala
Lillian Riddick
Barbara Robbertse
Brian Smith-White
Pooja Strope
Anjana Vatsan
David Webb

GDV/Remap/GBench
Valerie Schneider
Peter Meric
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NCBI Genome Resources Workshop

Time	Topic
12:50 – 1:10	Submission of Genomes to GenBank *Karen Clark*
1:10 – 1:30	GEO Submissions and Usage *Steve Wilhite*
1:30 – 1:55	From Annotation to Visualization: Exploring Genes and Genomes with NCBI Tools *Eric Cox*
1:55 – 2:15	Programmatic Access to Genomic Data: E-Utilities and FTP *Vamsi K. Kodali*
2:15 – 2:35	NCBI Resources for Phyletically-Defined Next Generation Analysis in and out of the Cloud (a.k.a. Cool New Stuff!) *Ben Busby*
2:35 – 3:00	Q & A session